A Universal System for the Diagnostic Evaluation of Biomedical Signals

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In vivo diagnostic procedures are leading to the collection of signals related to the bodily functions (ECG, EEG, EMG etc.), and the evaluation and assessment of the individual patient. On the other hand, several in vitro diagnostic procedures, as Electrophoresis or Chromatography produce also "signals" that correspond to certain physiological states or indicate abnormalities or diseases.

The evaluation of the data collected and the individual assessment of the patient depend on the various theoretical models of disease adopted at the time and an additional problem arises out of the difficulty of establishing criteria of normality and abnormality in human biology.

The typical methodological approach to obtain a diagnostic conclusion is the comparison of the data-set collected from the patient with a similar "reference"-set of data, which represents the "normal" condition and which is defined in a more or less arbitrary manner being based on previous -and collective- experience. The difference of the sets constitutes the "symptoms"-set, which is intended to lead to the successful diagnosis.

Therefore, a Universal Biomedical Signal Acquisition and Processing System, including A/D converting interfaces has been developed, suitable for in vivo electrical (ECG, EEG etc.) and non-electrical (lung and respiratory noises etc.) Biosignals. Printed-out Biosignals as well as, Electrophoretic and Chromatographic Patterns may be digitized and introduced through a scanner, allowing for in vitro and off-line data acquisition.

A "diagnostic vector" $\mathbf{d}_j = \mathbf{dj}\ (a_{1j}, a_{2j},...,a_{kj})$ mathematically quasi equivalent to the acquired waveform including k diagnosis-relevant information items akj of the j-th patient is formed and compared to a set of i diagnostic vectors $\mathbf{D}_i = \mathbf{D}_i\ (a_{1i}, a_{2i},...,a_{ki})$, i = 1,2,...,m, which constitute a reference knowledge base and which are correlated to a diagnostic indication. According to a "case based reasoning" procedure, $\mathbf{D}_j$ is compared to a large number of vectors $\mathbf{D}_k$, occurring from already evaluated cases (i.e. electrical Biosignals, Electrophoretic gels, Chromatograms etc.), which constitutes the continuously expandable "knowledge base". By defining a comparison metric M, for the n-th patient, a diagnostic proposal is displayed by the system, by appointing to that case, the proposal attached to the vector **Di** that minimizes the metric $M(\mathbf{d}_j\text{-}\mathbf{D}_i), i=1,2,...,k$.

A Turbo Pascal® 7.0 programmed algorithm is used the real time formation and the handling of Biosignals and other in vivo Parameters Knowledge Bases. The scanned patterns are processed using a C++Visual® programmed custom-made application. At the time, ECG (in vivo and print-outs) and Thermal Conductivity based Respiratory Curve acquisition and evaluation are available.

The System enables further applications in the Operating Room as EEG-assisted anesthesia monitoring , based on the evaluation of the power spectrum of an intra-operative EEG or transfer line resonance overshoot correction during invasive Arterial Pressure Monitoring in the ICU etc.

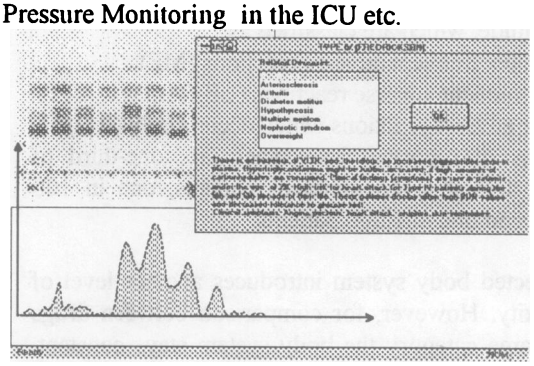

Figure 1 - A typical active window during a Lipoprotein-Electrophoresis Gel evaluation.

Decision Support focused on Lipoprotein Gels automated diagnosis has been completely developed. The Knowledge-Base was formed by introducing into the system 104 evaluated gels, kindly provided by Prof. Dr. H. Schmidt-Gayk, University of Heidelberg. A further extension to include Abnormal Hemoglobin Electrophoresis and Thin Layer Chromatography evaluation algorithms is under development .

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